

NCBI

CD-Search

Entrez ?

RPS-BLAST 2.2.1 [Apr-13-2001]

Query=

(553 letters)

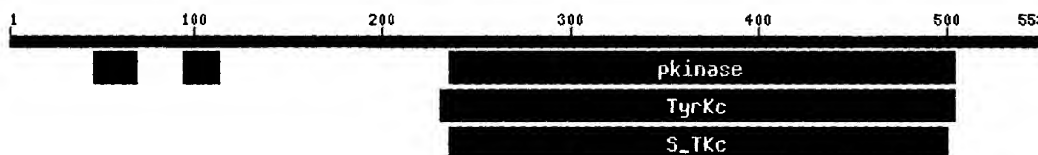
RECEIVED

SEP 07 2001

TECH CENTER 1600/2900

- .. This CD alignment includes 3D structure. To display structure, download [Cn3D v3.00!](#)

Mouse-over boxes to display more information



PSSMs producing significant alignments:

Score E
(bits) value

- [gnl|Pfam|pfam00069](#) pkinase, Protein kinase domain 180 2e-46
- [gnl|Smart|smart00219](#) TyrKc, Tyrosine kinase, catalytic domain; Phosphotransferases.... 161 8e-41
- [gnl|Smart|smart00220](#) S_TKc, Serine/Threonine protein kinases, catalytic domain; Pho... 160 2e-40
- [gnl|Smart|smart00366](#) LRR_PS, Leucine-rich repeat, plant-specific subfamily 38.5 0.001
- [gnl|Smart|smart00366](#) LRR_PS, Leucine-rich repeat, plant-specific subfamily 36.6 0.004

- [gnl|Pfam|pfam00069](#), pkinase, Protein kinase domain.

Add query to multiple alignment, display sequences

CD-Length = 256 residues, 97.3% aligned
Score = 180 bits (457), Expect = 2e-46

```

Query: 235 ILGRGGFGKVYKGR-ADGSLVAVKRLKEERTPGGELQFQTEVEMISMAVHRNLLRLRGF 293
Sbjct: 6   KLGSGAFGKVYKGHKDTGEIVAIIKKRSLSEKKRFLREIQILRRLSHPNIVRLLG 65

Query: 294 CMTPTERLLVYPYMANGSVASCLRERQPSSEPPLDWPTRKRIALGSARGLSYLHDHCDPKI 353
Sbjct: 66 FEEDDHLYLVMEYMEGGDLFDYLRRN---GLLLSEKEAKKIALQILRGLEYLHSR---GI 119

Query: 354 IHRDVKAANILLDEEFVAVVGDFGLARLMDYKDTHTTAVRGTLGYIAPEYLSGKSSEK 413
Sbjct: 120 VHRDLKPENILLDENGTVKIADFLARKLESSYEKLTTFVGTPEYMAPEVLEGRGYSSK 179

Query: 414 TDVFGYGIMLLELITGQRAFDLARLANDDDVMLLDWVKSLLKEKKLEMLVDPDLENNYID 473
Sbjct: 180 VDVWSLGVILYELLTGKLPFP--GIDPLEELFRIKE-----RPRLRLPLPP 223

Query: 474 TEVEQLIQVALLCTQGSPMERPKMSEVVRML 504
Sbjct: 224 NCSEELKDLIKCLNKDPEKRPTAKEILNHP 254

```

[gnl|Smart|smart00219](#), TyrKc, Tyrosine kinase, catalytic domain; Phosphotransferases. Tyrosine-specific kinase subfamily.

[Add](#) query to multiple alignment, display sequences

CD-Length = 258 residues, 99.6% aligned
Score = 161 bits (408), Expect = 8e-41

Query:	231	TFSTILGRGGFGKVYKGR	LADGS----	LVAVKRLKEERTPGGELQFQTEVEMISMAVHRN	286
Sbjct:	2	TLGKKLGEGAFGEVYKGT	LKGKGGVEVAVKTLKEDASEQQIEEFLREARLMRKLDPN	61	
Query:	287	LLRLRGFCMTPTTERLLV	PYPMANGSVASCLRERQ	PSEPPLDWPTRKRIALGSARGLSYLH	346
Sbjct:	62	IVKLLGVCTEEEP	LMIVMEYMEGGDLLDYLRKNRPKE--LSLSDLLSFALQIARGMEYLE	119	
Query:	347	DHCDPKIIHRDVKAANILL	DEEFAVVGDFGLARLMDYKDTHVTTAVRGT-LGYIAPEYL	405	
Sbjct:	120	SK---	NFVHRDLAARNCLVGENKTVKIADFG	LARDLYDDYYRKKKSPRLPIRWMAPESL	176
Query:	406	STGKSSEKTDVFGYGIMLLE	LIT-GQRAFDLARLANDDDVMLLDWVKSLLKEKKLEMLVD	464	
Sbjct:	177	KDGKFTSKSDVWSFGVLLWEI	FTLGESPY--PGMSNEE-----VL	214	
Query:	465	PDLENNY----	IDTEVEQLIQVALLCTQGSPMERPKMSEVVRML	504	
Sbjct:	215	EYLKKGYRLPQPPNCPDEIYD	MLQCWAEDPEDRPTFSELVERL	258	

● [gnl|Smart|smart00220](#), S_TKc, Serine/Threonine protein kinases, catalytic domain; Phosphotransferases. Serine or threonine-specific kinase subfamily.

[Add](#) query to multiple alignment, display sequences

CD-Length = 256 residues, 95.7% aligned
Score = 160 bits (405), Expect = 2e-40

Query:	235	ILGRGGFGKVYKGR-LADGS	LVAVKRLKEERTPGGELQ-FQTEVEMISMAVHRNLLRLRG	292
Sbjct:	6	VLGKGAFGKVYLARDKKTG	KLVAIKVIKKEKLKKKKRERILREIKILKKLDHPNIVKLYD	65
Query:	293	FCMTPTTERLLVYPYMAN	GSVASCLRERQSEPPLDWPTRKRIALGSARGLSYLHDHCDPK	352
Sbjct:	66	VFEDDDKLYLVMEYCEG	DLFDLLKKR----GRLSEDEARFYARQILSALEYLHSQ---G	118
Query:	353	IIHRDVKAANILLDEEFA	VVGDFGLARLMDYKDTHVTTAVRGT	412
Sbjct:	119	IIHRDLKPENILLSDGHV	KLADFLAKQLDSGGTLLTTFV-GTPEYMAPEVLLGKGYGK	177
Query:	413	KTDVFGYGIMLLELITG	QRAFDLARLANDDDVMLLDWVKSLLKEKKLEMLVDPDLENNYI	472
Sbjct:	178	AVDIWSLGVILYELLTG	KPPFP----GDDQLLALFKKI-----GKPPPPFPPEWKI	225
Query:	473	DTEVEQLIQVALLCTQG	SPMERPKMSEV	500
Sbjct:	226	SPEAKDLIK---KLLVKD	PEKRLTAEEA	250

[gnl|Smart|smart00366](#), LRR_PS, Leucine-rich repeat, plant-specific subfamily

[Add](#) query to multiple alignment, display sequences

CD-Length = 24 residues, 100.0% aligned
Score = 38.5 bits (88), Expect = 0.001

CD-Search Results

Query: 46 LTNLVSLDLYMNSFSGPIPDTLGK 69
Sbjct: 1 LTSLQVLDLSNNNLSGEIPESLGN 24

gnl|Smart|smart00366, LRR_PS, Leucine-rich repeat, plant-specific subfamily

Add query to multiple alignment, display sequences

CD-Length = 24 residues, 83.3% aligned
Score = 36.6 bits (83), Expect = 0.004

Query: 94 ITTLQVLDLSNNRLSGPVPD 113
Sbjct: 1 LTSLQVLDLSNNNLSGEIPE 20

32

NCBI CD-Search Entrez ?

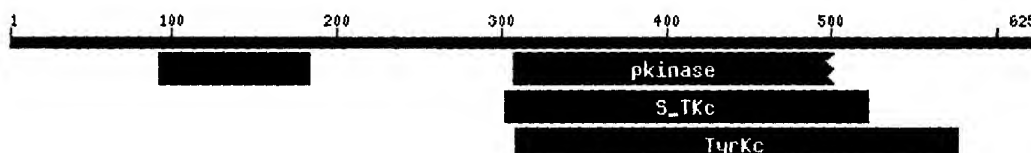
RPS-BLAST 2.2.1 [Apr-13-2001]

Query=

(625 letters)

- .. This CD alignment includes 3D structure. To display structure, download [Cn3D v3.00!](#)

Mouse-over boxes to display more information



PSSMs producing significant alignments:

Score E
(bits) value

- [gnl|Pfam|pfam00069](#) pkinase, Protein kinase domain [177](#) 2e-45
- [gnl|Smart|smart00220](#) S_TKc, Serine/Threonine protein kinases, catalytic domain; Pho... [160](#) 1e-40
- [gnl|Smart|smart00219](#) TyrKc, Tyrosine kinase, catalytic domain; Phosphotransferases.... [156](#) 3e-39
- [gnl|Smart|smart00366](#) LRR_PS, Leucine-rich repeat, plant-specific subfamily [39.3](#) 6e-04
- [gnl|Smart|smart00366](#) LRR_PS, Leucine-rich repeat, plant-specific subfamily [38.1](#) 0.001
- [gnl|Smart|smart00366](#) LRR_PS, Leucine-rich repeat, plant-specific subfamily [37.7](#) 0.002
- [gnl|Smart|smart00366](#) LRR_PS, Leucine-rich repeat, plant-specific subfamily [35.4](#) 0.009

- [gnl|Pfam|pfam00069](#), pkinase, Protein kinase domain.

Add query to multiple alignment, display sequences

CD-Length = 256 residues, only 74.6% aligned
Score = 177 bits (449), Expect = 2e-45

Query: 307 ILGRGGFGKVYKGR-ADGTLVAVKRLKEERTPGGELQFQTEVEMISMVHRNLLRLRGF 365
Sbjct: 6 KLGSGAFGKVYKGKHKDTGEIVAIKILKKRSLSEKKRFLREIQILRRLSHPNIVRLGV 65

Query: 366 CMTPTERLLVYPYMANGSVASCLRERPPSQPPLDWPTRKRIALGSARGLSYLHDHCDPKI 425
Sbjct: 66 FEEDDHLVLMMEYMEGGDLFDYLRRNGL---LLSEKEAKKIALQILRGLEYLHSR---GI 119

Query: 426 IHRDVKAANILLDEEF EAVVGDFGLAKLMDYKDTHTTAVRGTTIGHIAPEYLSSTGKSSEK 485
Sbjct: 120 VHRDLKPENILLDENGTVKIDFGLARKLESSSYEKLTTFTVGTPEYMAPEVLEGRGYSSK 179

Query: 486 TDVFGYGIMLLELITGQ 502
Sbjct: 180 VDVWSLGVILYELLTGT 196

gnl|Smart|smart00220, S_TKc, Serine/Threonine protein kinases, catalytic domain;
Phosphotransferases. Serine or threonine-specific kinase subfamily.

Add query to multiple alignment, display sequences

CD-Length = 256 residues, 82.4% aligned
Score = 160 bits (406), Expect = 1e-40

```
Query: 302 FSNKNILGRGGFGKVYKGR-LADGTLVAVKRL-KEERTPGGELQFQTEVEMISMAVHRNL 359
Sbjct: 1 YELLEVLGKGAFGKVYLARDKKTGKLVAIKVIKKEKLKKKKRERILREIKILKKLDHPNI 60

Query: 360 LRLRGFCMTPTERLLVYPYMANGSVASCLRERPPSQPPLDWPTRKRIALGSARGLSYLHD 419
Sbjct: 61 VKLYDVFEDDDKLYLVMEYCEGGDLFDLLKKRGR----LSEDEARFYARQILSALEYLHS 116

Query: 420 HCDPKIIHRDVKAANILLDEEFEAVVGDFGLAKLMDYKDTHTVTTAVRGTIGHIAPEYLS 479
Sbjct: 117 Q---GIIHRDLKPENILLDSDGHVKLADFGGLAKQLDSGGTLLTTFV-GTPEYMAPEVLLG 172

Query: 480 GKSSEKTDVFGYGIMLLELITGQRAFDLARLANDDDVMLLDWV 522
Sbjct: 173 KGYGKAVDIWSLGVILYELLTGKPPFP----GDDQLLALFKKI 211
```

gnl|Smart|smart00219, TyrKc, Tyrosine kinase, catalytic domain; Phosphotransferases. Tyrosine-specific kinase subfamily.

Add query to multiple alignment, display sequences

CD-Length = 258 residues, 97.7% aligned
Score = 156 bits (395), Expect = 3e-39

```
Query: 308 LGRGGFGKVYKGR-LADG----TLVAVKRLKEERTPGGELQFQTEVEMISMAVHRNLLRLR 363
Sbjct: 7 LGEGAFGEVYKGTLLKGGGVEVEVAVKTLKEDASEQQIEEFLREARLMRKLDHPNIVKLL 66

Query: 364 GFCMTPTERLLVYPYMANGSVASCLRERPPSQPPLDWPTRKRIALGSARGLSYLHDHCDP 423
Sbjct: 67 GVCTEEEPMLIVMEYMEGGDLLDYLRKNRP--KELSLSDLLSFALQIARGMEYLESK--- 121

Query: 424 KIIHRDVKAANILLDEEFEAVVGDFGLAKLMDYKDTHTVTTAVRGT-IGHIAPEYLS 482
Sbjct: 122 NFVHRDLAARNCLVGENKTVKIADFGGLARDLYDDDYRKKKSPRLPIRWMAPESLKDGKF 181

Query: 483 SEKTDVFGYGIMLLELIT-GQRAFDLARLANDDDVMLLDWVKGLLKEKLEMLVDPDLQT 541
Sbjct: 182 TSKSDVWSFGVLLWEIFTLGESPY-----PGMSNEEVLEYLKKGYRLPQPPNCPDE---- 232

Query: 542 NYEERELEQVIQVALLCTQGSPMERPKMSEVVRML 576
Sbjct: 233 -----IYDLMLQCWAEDPEDRPTFSELVERL 258
```

gnl|Smart|smart00366, LRR_PS, Leucine-rich repeat, plant-specific subfamily

Add query to multiple alignment, display sequences

CD-Length = 24 residues, 100.0% aligned
Score = 39.3 bits (90), Expect = 6e-04

```
Query: 92 LKNLQYLELYSNNITGPIPSNLGN 115
Sbjct: 1 LTSLQVLDLSNNNLSGEIPESLGN 24
```

gnl|Smart|smart00366, LRR_PS, Leucine-rich repeat, plant-specific subfamily

Add query to multiple alignment, display sequences

CD-Length = 24 residues, 100.0% aligned
Score = 38.1 bits (87), Expect = 0.001

Query: 116 LTNLVSLDLYLNSFSGPIPESLGK 139
Sbjct: 1 LTSLQVLDLSNNNLSGEIPESLGN 24

gnl|Smart|smart00366, LRR_PS, Leucine-rich repeat, plant-specific subfamily

Add query to multiple alignment, display sequences

CD-Length = 24 residues, 100.0% aligned
Score = 37.7 bits (86), Expect = 0.002

Query: 140 LSKLRFLRLNNSLTGSIPMSLTN 163
Sbjct: 1 LTSLQVLDLSNNNLSGEIPESLGN 24

gnl|Smart|smart00366, LRR_PS, Leucine-rich repeat, plant-specific subfamily

Add query to multiple alignment, display sequences

CD-Length = 24 residues, 83.3% aligned
Score = 35.4 bits (80), Expect = 0.009

Query: 164 ITTLQVLDLSNNRLSGSVDP 183
Sbjct: 1 LTSLQVLDLSNNNLSGEIPE 20

31 Aug. 2001

Sequence Data

Page 1

Molecule: 37

NoName, 2072 bps DNA

Description:

File Name: seq id 32.cm5, dated 31 Aug 2001

Printed: 195-2072 bps, format Translated, Frame 3

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195  atggagtcga gttatgtggt gtttatctta ctttcactga tcttacttcc
      M E S S Y V V F I L L S L I L L
245  gaatcattca ctgtggcttg cttctgctaa tttggaagggt gatgctttgc
      P N H S L W L A S A N L E G D A L
295  atactttgag ggttactcta gttgatccaa acaatgtctt gcagagctgg
      H T L R V T L V D P N N V L Q S W
345  gatcctacgc tagtgaatcc ttgcacatgg ttccatgtca cttgcaacaa
      D P T L V N P C T W F H V T C N
395  cgagaacagt gtcataagag ttgatttggg gaatgcagag ttatctggcc
      N E N S V I R V D L G N A E L S G
445  atttagttcc agagcttgggt gtgctcaaga atttgcagta tttggagctt
      H L V P E L G V L K N L Q Y L E L
495  tacagtaaca acataactgg cccgattcct agtaatcttg gaaatctgac
      Y S N N I T G P I P S N L G N L
545  aaacttagtg agtttggatc tttacttaaa cagcttctcc ggtcctattc
      T N L V S L D L Y L N S F S G P I
595  cggaatcatt gggaaagctt tcaaagctga gatttctccg gcttaacaac
      P E S L G K L S K L R F L R L N N
645  aacagtctca ctgggtcaat tcctatgtca ctgaccaata ttactaccct
      N S L T G S I P M S L T N I T T
695  tcaagtgtta gatctatcaa ataacagact ctctggttca gttcctgaca
      L Q V L D L S N N R L S G S V P D
745  atggctcctt ctcaactctt acacccatca gttttgctaa taacttagac
      N G S F S L F T P I S F A N N L D
795  ctatgtggac ctgttacaag tcacccatgt cctggatctc ccccgttttc
      L C G P V T S H P C P G S P P F
845  tcctccacca ctttttattc aacctcccc agtttccacc ccgagtgggt
      S P P P P F I Q P P P V S T P S G
895  atgggtataac tggagcaata gctgggtggag ttgctgcagg tgctgctttg
      Y G I T G A I A G G V A A G A A L
945  ccctttgctg ctcttgaat agcctttgct tgggtggcgac gaagaagccc
      P F A A P A I A F A W W R R R S
```

995 actagatatt ttcttcgatg tccctgccga agaagatcca gaagttcatc
P L D I F F D V P A E E D P E V H

1045 tgggacagct caagagggtt tctttgcggg agctacaagt ggcgagtgat
L G Q L K R F S L R E L Q V A S D

1095 gggtttagta acaagaacat ^{the}tttgggcaga ggtgggtttg ggaaagtcta
G F S N K N I L G R G G F G K V

1145 caagggacgc ttggcagacg gaactcttgt tgctgtcaag agactgaagg
Y K G R L A D G T L V A V K R L K

1195 aagagcgaac tccaggtgga gagctccagt ttcaaacaga agtagagatg
E E R T P G G E L Q F Q T E V E M

1245 ataagtatgg cagttcatcg aaacctgttg agattacgag gtttctgtat
I S M A V H R N L L R L R G F C

1295 gacaccgacc gagagattgc ttgtgtatcc ttacatggcc aatggaagtg
M T P T E R L L V Y P Y M A N G S

1345 ttgcttcgtg tctcagagag aggccaccgt cacaacctcc gcttgattgg
V A S C L R E R P P S Q P P L D W

1395 ccaacgcgga agagaatcgc gctaggctca gctcgagggt tgtcttacct
P T R K R I A L G S A R G L S Y

1445 acatgatcac tgcgatccga agatcattca ccgtgacgta aaagcagcaa
L H D H C D P K I I H R D V K A A

1495 acatcctctt agacgaagaa ttcgaagcgg ttgttgaggaga tttcgggttg
N I L L D E E F E A V V G D F G L

1545 gcaaagctta tggactataa agacactcac gtgacaacag cagtccgtgg
A K L M D Y K D T H V T T A V R

1595 caccatcggt cacatcgctc cagaatatct ctcaaccgga aaatcttcag
G T I G H I A P E Y L S T G K S S

1645 agaaaaccga cgttttcgga tacggaatca tgcttctaga actaatcaca
E K T D V F G Y G I M L L E L I T

1695 ggacaaagag ctttcgatct cgctcggcta gctaacgacg acgacgtcat
G Q R A F D L A R L A N D D D V

1745 gttacttgac tgggtgaaag gattgttgaa ggagaagaag ctagagatgt
M L L D W V K G L L K E K K L E M

1795 tagtggatcc agatcttcaa acaaactacg aggagagaga actggaacaa
L V D P D L Q T N Y E E R E L E Q

1845 gtgatacaag tggcgttgct atgcacgcaa ggatcaccaa tggaaagacc
V I Q V A L L C T Q G S P M E R

KINASE
DOMAIN
SEQ ID
NO 32

NoName 32

1895 aaagatgtct gaagttgtaa ggatgctgga aggagatggg cttgoggaga
P K M S E V V R M L E G D G L A E

1945 aatgggacga atggcaaaaa gttgagattt tgagggaaga gattgatttg
K W D E W Q K V E I L R E E I D L

1995 agtcctaata ctaactctga ttggattctt gattctactt acaatttgca
S P N P N S D W I L D S T Y N L

2045 cgccgttgag ttatctgggc caaggtaa
H A V E L S G P R -

Reference molecule: NoName 1020 - 1684 (665 bps) Homology

Sequence 2: NoName 3304 - 4081 (778 bps) 100%

Alignment type: Local (FastScan)

Homology details: Percent Max 78; Score 522; Length 665

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NoName 32 ( 1020) gccgaagaagatccagaagttcatctgggacagctcaagagggttttctttgcgggagcta
NoName 20 ( 3304) .....
NoName ( 1080) caagtggcgagtgatgggttagtaacaagaacattttgggcagagggtgggttgggaaa
NoName ( 3364) .....
NoName ( 1140) rgtctacaagggacgcttggcagacggaactcttggtgctgtcaagagactgaaggaagag
NoName ( 3424) .....
NoName ( 1200) cgaactccaggtggagagctccagtttcaaacagaagtagagatgataagtatggcagtt
NoName ( 3484) .....
NoName ( 1260) catcgaaacctgttgagattacgaggtttctgtatgacaccgaccgagagattgcttgtg
NoName ( 3544) .....
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NoName ( 3604) .....gtaaaaactaaacaatt
NoName ( 1363) -----
NoName ( 3664) aaacatcttggtgctctctctcaattactttgacgtgaagtgttttttcatgttttccttt
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NoName ( 3724) atgggttcataattgttggttacactaatgacacag.....
NoName ( 1387) ttgattggccaacgcggaagagaatcgcgctaggctcagctcgagggttgccttacctac
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NoName ( 1507) acgaagaattcgaagcggttgttgagatttcgggttgcaagcttatggactataaag
NoName ( 3904) .....a.....
NoName ( 1567) acactcacgtgacaacagcagtcggtggcaccatcggtcacatcgctccagaatatctct
NoName ( 3964) .....
NoName ( 1627) caaccgaaaaatcttcagagaaaaccgacgttttcggatacggaatcatgcttctaga
NoName ( 4024) .....1684
4081
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